

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACTT
CCAGAAAACAACCCTTTTTGTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFSGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCACTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCAATTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG
TTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTCTTCTGGAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTAAAACTTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAACGGATCCTGTGACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTTGGTCCCAACACATTTCTTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCTGCTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA
GATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAACAACAAAATGCTATGGTAGC
ATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAAGTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAAGGCGGAGAGGAGCCAAAGGTAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTAAAGGTTACATGGAAAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV
LNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLEFSCLLWLTFMYFFWKLGP
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDAL EELSRO
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCTCTAG
 GATTAGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
 ATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACAGAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCTACTACTACTCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG
 GAACTAGCACCATGTCTCAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGTCTCTCTCTTTGGTGCTG
 CAGCTGGTCTTGGATTTTGTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAACAAGAAT
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA
 TGAGGAATCAAAGAAAACCTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC
 GATGCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
 CATGCTCCTTACCCTGCCCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAGAAAGTCCA
 CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAT
 GCCCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAAGTGCAAGGAC
 CTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAAT
 GGCAGAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAAT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAACTT

FIGURE 6

MARCFSLVLLLSIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN
SSDTWTNSCIPELIITTKDPIENTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNNEESKKTDKNPESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGGC
GGCTCCCGGCGGGAGCGAGCAGATCCAGTCCGCCCCGACGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCCTGCTGTGCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCG
GCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC
TGGACAAATGGTCTTTTTCAGAGACAGTTATCAGATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGAGAGCA
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCAGCT
CCCCAGGCTGTTCTCCAGGCTTTCAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAACTGCA
GGAGCAGTTTGGCAACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAATG
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGG
AGGGGTGCTATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACTAATTCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTATCCAGAGTTCCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPOEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEAAAAKASSEVNLANLP SYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRM LCTR DSECCGDQLCVWGH
TKMATRG SNGTICDNQRDCQPG LCCAFQ RGLLFPVCTPLPVEGELCHDFASRLDLITWELEPDG
ALDRCP CASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE
RSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCACCTTGTGAACCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCAAAG
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCTT
AACTGGGTACTGGCCCTGGGCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATTGGCATTGAGGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGTTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTCGTCCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGTCTGTCTCTTTCTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT
GTCATCGCCAGCGCTTCTTCAGCGTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTtagGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAAA
AAGATTTTATTAAAGATATTTTGTTAACTC

FIGURE 10

RTGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFGQYSSKGLIQRSVFNLQIYGVLGLEFWTL
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAKNAFMLLMRN
IVRVVLDKVTDLLLFFGKLLVVGVGVLSTFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
CAGCCGCAACTCCACCGTGAGCCGCTCATCTTCAGTTCTTCCTCTTCCTGGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGGCTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGC
GGGATCCCCACCGTCTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTCTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCA
GCCGGGACCCCCGGGCTGCCATCCAGAATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCCTC
ACCGTGGGTGCCTTTACATCCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGTCTGTGG
CTCCTTCTCTTTCATCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAAGCGGT
GGCTGGGCAAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTCACTCTCCTC
TTCTACTTGCTGTGATCGCGCCGCTGGCGCTGATGTTTCATGTACTACACTGAGCCCAAGCGGTGCCA
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGCTG
CCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTATCACCCCTCTACACCATG
TTTGTACCTGGTGCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
TGGGCCTCATCATCTTCTCTGTGACCCCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGT
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
ACTTCTGCCTGGTGTGCTGGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCTCA
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGCTGCTGGAGAGAGCGGGGAACCTCCACACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCAGTCCCCAGGGGACCCTGCCCCCTTCTG
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCGGTGTAACAAAAA

FIGURE 12

MGACLGACSLSCASCLCGSAPCILSCCPASRNSTVSRLIFTFFFLGLVLSIIMLSPGVESQL
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLFCVCVSIAAVLPKV
QDAQNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVWKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGGCCGGCCAGGAACCACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTGTCACCTTTGACCTCTTATTCTGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCAATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTCATTTCATC
CTTGCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTAAATGTGAAAAACCCCTCAGAGAAAGTC
ATCGAGGCCAAAAAGAGGCAGGAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTTCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAATAGGTGAAGAAAGTCTTGTGCTGTATTCCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTAC
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTGTTTGCATTATGTGTATGGCCTGAAGTGTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTTCATATCATGTTTCCTTTCGCTTCAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG
CCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCGCCGCCCTCCCGGGACAGAAGATGTGCTCCAG
GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGGGCTGCCCAT
CCGGCTGCCAGTGACGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCC
CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
AGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTACAGAACCAGATCGCCAGCC
TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
CCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCGCCTGCTGCTGCTGGACCTCAGC
CACAACAGCCTCCTGGCCCTGGAGCCCGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
GGCTGGTCTGGGGTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACG
CGCCTGCGGCTGCGCGGCAACACCCGATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGCG
TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCTGCAGGCCCTGCGTGGCGACCTCTCGGGCC
TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTCAACTGCGTGTGCCCCCTGAGC
TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTGCGCCAGCCCTGAGGAGACGCGCTGCCA
CTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAG
CCACCACCACACGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCT
TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCGCCACTGAGGCCCCAGCCCGCCCTC
CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
ATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACG
GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTACAGCCGAG
GCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
GGCCCTGATAAGCGGTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTACCCCA
GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCGGGCGGGTGCCGGAGG
GCGAGGAGGCTGCGGGGAGGCCATACACCCAGCCGCTCCACTCCAACCACGCCCCAGTCAAC
CAGGCCCGGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
GCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCAGG
ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCGGAAGTGGAGGGAGTGAAGTCCCCCTGGAG
CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
ACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAGCCCTACATCTAAGCCA
GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
CTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
CCTGGGCACGGCGGGCCCTGCCATGTGTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC
TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGTCCCGGAAGAGCAGAGGGAGAGCGGGTAGGC
GGCTGTGTGACTTAGTCTTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCT
GGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATATGAA
GGCCTTTTGTAGAAAAAATAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP LLLPL LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M Q G T R P S P T P
V T P R P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S I A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E G V K V P L E P G P K A T E G G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAATGAAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
CTTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCAAAGGCTCTTGTATATTATACAT
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTTAGTGAAGGCT
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTTCAGCTTTCATGATC
CAGATTTGCTTGTATTAAAGACCAATATTCAGTTGAACCTCCTTCAAATTCCTGTTAATGGATAT
AACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACAATTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAAATATTTGCAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG
TTTTTTACTTTTCATGATTGGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG
AAGATTAACCTATTTTTAATAAAATTTATGTCTAAGATTAAAAA
AAA

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPFLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMQEAEEMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLIAMVLSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAAGCCCATTCTGCAGTGGAATTCATGAAGTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT
CCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAA
AGTCTAGACAACTGAAAGGCAATAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAGAACACATCTCCTTTTCAACCCATTCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCTGCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEGKLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFENDSLRRDMK
AFGVHVSCIEPGLFKNLADFPVKVIEKKLAIWEQLSPDIKQYGEYIEKSLDKLKGKNSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTCTTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATCCGT
CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGCAAGGAGCATTT
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACCTGGGTATAAACTGTATCAGGTCCTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA
GAAAAGGAGAGGAGCACAGATTGAGGACGAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA
ACATTTTTCTTTGTGTCAGGCATTACGGACCTTTTTTCCAAATTCTGAATTCTTCATTATGTGTT
ATGTCTTTAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACTACAACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
GAGCAGCCCAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTTGATCCTTTTAACCTTACAAGGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTTACC
TGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAAAAATAAAATGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA
GCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCTCTGCGGTCCCCGCGGCGCCTGCCACCTTCCCTCCCTCCCC
GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCGTGCCTCGCGGAAACCCGAGGTCAACAGCCGCGGCTCT
GCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCGCGCCTGGCACCGGGACCGTTGCGCTGA
CGCGAGGCCAGCTCTACTTTTCGCCCCGCGCTCTCCTCGCCTGCTCGCTCTTCCACCAACTCCAACCTCCTTCTCC
TCCAGCTCCACTGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCGGTAGCGCGCTTCCGTCGGTCCCAA
GGTGGGAACGCGTCCGCCCCGCGCCGACCAATGGCACGGTTGCGCTTGCCGCGCTTCTCTGCACCTGGCAGTGCTC
AGCGCCGCGTGTGGTGGCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGGACGCTTTACGTGTCCAAGGCTTC
AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT
CAAGAGATGGAGGAGAAGTACAGCTGCAAGTAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
CAAGCTGTCTTTGCTTACGTTACAAGAAGTTGATGAATTCTTCAAAGAATACTTGAAAATGCAGAGAAATCCCTG
AATGATATGTTTGTGAAGACATATGGCCATTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATG
TTCCGCTGTGTAAGTCCAGTACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
CCCTTCGGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTAAGTTTCTGCTCAAGGC
TTAGCGGTTGCGGGAGATGTGCTGAGCAAGGCTCTCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG
ATGATCTACTGCTCCACTGCGGGGCTCTGCTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGC
TGTTTGCCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
GAGGCTCCTTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATATGAACATGCAGGAT
AATAGTGTTCAAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
TCCATCTCTGAAAGTGCCCTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACCACAGCAGCTGGCACT
AGTTTGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCCCTCCCTCCGAGCAAC
GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
CTGTTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAAACCAGAC
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGAGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGAGAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGCTCTGGGGCA
CAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTCTGAG
AAAAAGTGTTTCATCAAAAAGTTAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTCAGTTTTGGG
AGGAAAAGGGACTGTGCATTGAGTTGGTCTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTGTTTGTATGTTTTTTCTCATTTGTTTGTGGGTT
TTTTTTTCCAACGTGATCTCGCTTGTTCCTACAAGCAACAGGGTCCCTTCTGGCACGTAAACATGTACGTATT
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAAGAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLKLVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQGC GPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGCGGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTCTGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAACTGTAGCTTCCT
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTTCACTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGCTG
CTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGAGGTGTGC
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC
GAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTA
GCAGAATGAGAGAAGACATTCATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC
CCAATGTTGTCCCTTTCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL
TGASGKVALLELGCCTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLCSSVQSPRKVLQEVRRVLRPGGVLFFWEHVAEPYGSWAFMWQQVFPEPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSPSSKALICSFPSL
QLEQATHQPIYLPRLGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCAAGCCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTCATTAAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2025-1-28

FIGURE 30

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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FIGURE 31

GTTCGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATAACACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCAAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCAGGTT
ATGGAAGGCGGCCAAGTGGAATATAAGCCCCTTTTCGGGCATTCCGTACATGTGGTCGTACCATT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCCTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAG
GATTCCGAGAATCATTGTGTATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGCCAAGAAGTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACCTTTCTGTGTTTTGCTGTTGATC
TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA
GGGAACAGAAGTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
TTAAAGACCTAATAAACCTATTCTTCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFA
ILIFFWVLWVAVLLSLGTAGAAQVMGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA
GAVVTCYFNRSKNPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVTPSALTYSSSKSPAQAGETTKAYQRPPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFOKP
VGADVSLGLVPKEELSTQSLFPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQQLLADVAQALDI
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLOPLVKRVCDTDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISDTRIGAVQYTYEQRLFEGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALQEL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAWAAQEELEVIATHPARHDSFF
VDEFNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

[illegible][illegible]

FIGURE 36

MASALWTVLP SRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNW MYFYEYEP IYRQDFHF
TLREHSNC SHQNPFLVILVTSHPSDV KARQAIRVTWGEKKS WNGYEVLTFFLLGQEA EKEDKMLA
LSLEDEHLLYGD IIRQDFLD TYNNTLKTIMAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYL
NLNHSEKEFFTGYPLIDNYSYRGFYQKTHISYQEY PFKVFP PYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLLKVN IHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCCCTTGCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCCTCTGCCCCGGAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGT
ACCTTGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTCCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGAAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGC
TAAACCTGGGTTTGTTCATCCAATAAGATTGTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCCTATCCAGAGCATAG
GATCCTCACTCCACGTCCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCTTGTTCATGACGGCAGCTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTTGGGGGCCAGTCAATGGGTACCAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGAGCCCATGCTAAATTTGGCACCCTGGTGTCTTTCTTTTGAACAACTCCTATGT
TCTTAGTGGCAATGAGAAAAAGCTTGGCAGCAGATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCCTGCCGA
GAACCAAGATTTCAGACCTGGTGAGAAGGAGTCTTCCGATGCAGGTTCACTCAAGGGAGACACCATACACAGCATAT
ACTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGGCCCTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTACCCCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCTGCATCCCTATCTGCGGGAATTTGAGAACATCACTGCTCCAAAGA
CCCAAGGTTGCGCTGGCGTGGCAGGAGCCATCTACAGGAGGACAGCGGGTGCATGACGGCAGCCTACCAAGGGAGC
GTGTTCTAGTCTGCAGCGTGCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATCTACCGGATGATGACCGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATTCTGCATCCCAACTATGACCCCATCTGCTTGATGCTGACATCGCCATCTGAAGCT
CCTAGACAAGGCGCTATCAGCACCAGTCCAGCCCATCTGCCTCGCTGCCAGTGGGATCTCAGCACTTCTTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACCTGCAGAGACAGGAGGCATCGCGGCTGTGCTCTCCGGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCTTCACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCCGTCTGTACGTGTGCTATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCCTGTGAACCTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGCTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGCTTCCCCAACTTTCACTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCCTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTT
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTAATAAAATAAGGCTTGGCTTCT
GAACTACAAAAA
AAAAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSLHVLFSHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRVLPQVQSRETPHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKIFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFAQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTAATC
 TGAAGGTTCTCAGTCAAATTCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
 TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTC
 TGGTCTTGCCCTTGCTCAGTCTCTGCTAACTACATTGACAATGTGGCAACCTGCACTTCTGTATTAGAACTCTGTA
 AAGGTGCCCTCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
 TCACAGCCAGGGTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCTTAATGACAGACGAGCTGGCTTAGACA
 ACCCTGCCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCACTGGACTCTGGCCGGAGCAACCGAATA
 GGGCAGGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA
 GGCAAAAGAGCGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAAATTCTGAAACACCACTGCCCCGTAAG
 TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAA
 GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG
 TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
 ACAACTACGCTGTGCGTCTCTTGGCGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCA
 GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
 CCGAGGACAGCTTGAATAAACTGGTGGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCG
 GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
 GCCCAGAAAGTGCGGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTGCTCCCGCCAGGTTCCGCGAGC
 GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACA
 CTCCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
 GCATGACCGTCCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCGGAGGAG
 TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTCAGCC
 GGAGTGAGGCAGTGGCATTATTGAAAAGAATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
 CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
 GGGTCATGTGGCTGGAATTACCACGGTCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
 TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATAACAATGGAACAAACCTTTTTTCATCAAAATCCATTGTTGAAGGAA
 CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGTCTCAATGGTAGAAGTACATCAGGAATGA
 TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
 TTTTATGAATCAATGATGGGTGAGGAGAAACAGAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC
 TTGTGAGTTTTTATATTTAAAGAAAGATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
 ACACCTCAGAAAATATGATTCAAAAAATTAAGTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTATTACTCTAC
 AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAACAATAAATGATTGATTGTATACCCCACTGAATT
 CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTTACAGCT
 AAAATATTTTTTAAATGCATTGCTGAGAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR
ALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRSQPDIFQEAGWNSNGSWSPG
PGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPYVISVEPGGVISRDGR
IKTGDILLNVGDVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNNHMAPP
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
CACCAGTAACACTTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
GACAACTGTCCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
TAAAAAGTTTAAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTTATATCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTGG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTGGGGAT
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGCCCCCTG
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACAGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCC
TGGATCTTTTGGTGATGTTTGAAGAAGTGAATCTTTGTTGCAATAATTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTCTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLTFFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWGGE
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG
CCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCAACAG
ACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCTCCC
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTGTTT
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FIGURE 44

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCCHRSKCGMCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCTCCATG
GTCCTCCTGTGTCTCCTGTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTtaggtctattgcttggttggaattctggaggtcctgtttgggct
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNPSNSNANCEFSL
KNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA
CATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTT
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCKYKS
SQKQHSPVPEKAIPITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
AGGACAGGGAGTCCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
AGGAGACCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
TTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG
GTGCCTTGGCCACAGTGGTGTCTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCCG
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
GGGCCACCAAATTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
CATAAACCCGGGTGTGAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGG
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTCTGGAA
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
GCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACTCCCTCCTTAA
AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA
AA
AA

FIGURE 52

MKFAQPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGKKAIGKEAGGAAGSKVS
EALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHGADAVRGSWQGVF
GHSGAWETSGGHGIFGSQGGGQGNPGLGTPWVHGYPGNSAGSFGMNPQAPWGQGGNGGPPNF
GTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGS
SSGSSSGSSSGGSSSGGSSSGNSGSGSRGDSGSESSWGSSTGSSSGNHGSGGGNGHKPGCEKPGNE
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGSGSDNYRGQGSWSGGGDAVGGVNTVNTSETSPGM
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCCACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCGCCGGCTCCAGTGTTC
CACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTGGCCACCTATCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGTGCCA
TTGCACCCAAGGATAATCTTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCTTCCATTTCAACATCCT
GAAGTCCATATAACGATCTTCAACAAGAGTGCAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTCAGGAGAGGGCCAGTGAATATATTGCCACCAT
CTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTCATCCGGGAGCGGCGTCGCACCTCCCCACTCAGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACACCACG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCAGGACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTCCGCA
GGGCCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPPKRNWFWGHLG
LITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDITRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDLDFIDVLLLSKDEDEGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCACTCTTTGGCATTGACGTGG
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCGGTGTGTCTTGC
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTGCTT
GTGATTTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGAATCTTCCTCATGTACCTGTTTCCTC
TCTGGATGTTGTCCCCTGAATCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA
AA

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCIIQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCACCAGCAGGCCGCCAATGCTCTGTCTGTGCCTG
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATCTCCACCTACCGCAGTGGGAAGCAGAAAATTGTACAGCT
GGAGATAAGGACCTTGATGGGACGTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAATTTCTAAGAGCATGGATAAAAACGGCAGCATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCCTCCACCCCGTGGAAAACATCCCCGAGATCATCCTCTACTGGAAGCATTCACG
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA
CACCTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCCATGCCCTCCCGCAGCAACAATGGGCATCGTTGGTGGCTTCACTCAGATGATTGAGAGAAGGAGGGGCCAGG
TCACTCTGGCGGGGCAATGGCATCAACGTCCTCAAAATTTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAG
ATCAAGCGCCTTTGGTAGTGACCCAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC
ATCGCCCGAGCAGCATCTACCAATGGAGTCCCTGAAGACCCGGATGGCGCTGCGGAAGACAGGCCAGTACTCAGGA
ATGTGAGTCTGCCCAGGAGGATCCTGGCCAGAGAGGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG
GGCATCATCCCTATGCCCGCATCGACCTTGCACTCTACGAGACGCTCAAGATGCTTGGCTGCAGCATGTGAGTG
AACAGCGCGGACCCCGGCTGTGTGTCTCTGGCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC
CCCCGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC
TTCAACATATCCTGCGGACCGAGGGGGCTTGGGCTGTACAGGGGGCTGGCCCCAATTCATGAAGTCTATCCCA
GCTGTGAGCATCAGCTACGTGGTCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTCCGCGTGAAGGGGAGGGC
CGCCCCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACACT
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCACCCGAGGGAGGGTGGGAGAGCTGGCAGGCCAGGGCTT
GTCCTGCTGACCCAGCAGACCTCCTGTTGGTTCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAGCAGG
CTCCGGGCTCAGATGTGTAAGGACAGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCTGGAGGCCGGCT
TAGTTCTTCCATTTACCCCTTGACCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC
CCTCTTGCTGCTGCTGTCTGCTGAGGTAAAGTGGGAGGAGGGCTACAGCCACATCCACCCCTCGTCCATCCC
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCTGACTTCCCAACCTACAGCATTGACGCCAATTTGGC
TGTGAAGGAAGAGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG
CTTGGGAGTGCAGGGGGCTCGGGCTGCCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGGGGCGAAGGGCAGAGCGCTTTGTGTCTTGGGGAGGGAAGGAAAGGTGTTGGAGGCCTTAATTATGG
ACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCCTGTCCAACCCAGCAGGGGCCAGC
GGGACCAGCCCCACATTCCACTTGTGTCACTGCTTGGAACTATTATTATTTGATTATTTGAACAGAGTTATGTCT
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCTATTTCAGTTTCAATTTTATTTATTTATTTATTTATTTATTT
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCCGCTGCAGTCACATCT
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTGGCTCCTTTCTTTGGCAG
GTTGGGAAGGGCTTGGCCCGAGCTTAGGATTTAGGGTTGACTGGGGGCTGGAGAGAGAGGGAGGAACCTCAAT
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCCAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG
TGAGGTGCCTCTCACTGTGAATTTGTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCCTCCCTCCAGC
CTTCTGCTGCCCTTGTAAATGCGGCGCACTGGCGACCTCACGGTTGCACTTCCATTCCACCAGAAATGACCTGA
TGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAAATTTGTTATATGAACATATAACTGGAGTCGTCAAAAAG
CAAATTAAGAAAGAAATGGACGTTAGAAGTTGTCTTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAA
AA

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG
QLDFEEFVHYLQDHEKKLRVLVFKILDKKNDGRIDAQEIIMQSLRDLGVKISEQQAEKILKSMKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG
AGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRNGINVLKIAPESAIAK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGOYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTGGCTTTTGGTATTTTCAAGGAGACACTCCATCACAGTCACTACTGTGCCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCTGATAT
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTGCGAGCAGGATGAAATGTTTCAAGGCCGACAGCAGTGTGTTGCTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAAGGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGA
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 60

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYLMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGAGGGGAGTATGGTAGT
GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAATCCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGAAGAACCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCCTACTGCCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGCCCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG
AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCTCACCAGGCCATCCTGTCAAACGAGCCATTTTCTCCAAAGTGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDP EAYSWFQSVDS DH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDEFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACCTTCGGGACC
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA
AGCGCTGCCTGAAGAACTCTTTACCTCTCCAGTGCCTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTCTCCGC
CCTCCTGGCTCTTCTTGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTAAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGLLLVLHLPGLFARSIGVVEEKVSONFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRSNSLGAGGKILSORP
PWSLIHRVLPDHPWGTLPNSVSWGGGGPGTGWGTREMPHPEGIWGINNQPPGTSWGNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGLPVLVLLLTLLGSSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

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FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGGCTGCCAACC CGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCACTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTAGAGGTTTGTTCCTCTTAGTCTGTGCCTGCTGCACCAG
 TCAAACTACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
 GATGAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
 TTTTTCCTCAAAATGTATCTATATTAATTCCTGAGAATTGGAGGAAAAATCCTCAGTACAAAAGGCCAAACATGAA
 AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA
 GAATGTGGAGAGAAAGGCGAATACATTCACTTCACTTCCCTGACCTTCTACTTGGAAAAAACAAAAATGAATATGGACCA
 CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTC
 TACCTGTCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
 CAAGGAGGCAAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAAGTATGGAAGAAAGTTGTCAATTCTTT
 CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTGTAAAGAA
 AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTAGAAGTACATGGGAGGTGATTAGCAAT
 TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTTGCTGAAGATCAGTCAA
 AGAATGTGTGCTTAGTCTTGTATAGTCTGGAAGCATGGGGGTAGGACCGCCTAAATCGAATGAATCAAGCAGCA
 AAACATTTCTGCTGCAGACTGTTGAAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
 AATAAGCTAATCCAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGA
 ACTTCCATCTGCTCTGGAATTAATATGCATTTCAAGTGATTGGAGAGCTACATTCCCACTCGATGGATCCGAAGTA
 CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTGAACAAAGTGGGGCCATTGTTTAT
 TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCAATTTTATGTT
 TCAGATGAAGCTCAGAACAATGGCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCGAGAAG
 TCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCTAATTTGATAGTACA
 GTGGGAAGGACACGTTCTTCTCATCATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCAGTGGAAACA
 ATAATGGAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAAAGTGGGCACT
 TGGGCATACAACTTCAAGCCAAAGCGAACCAGAAACATTAACTATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT
 GTGCCTCCAATCAGAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCGAGCCCAATGATTGTTTACGCAGAA
 ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
 TTGGAATTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
 ACAGAAAATGGCAGATATAGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTACGGCCTCCA
 CTGAATAGAGCGCGGTACATACAGGCTGGGTAGTGAACGGGGAAATTGAAGCAACCCGCCAAGACCTGAATTTGAT
 GAGGATACTCAGACCACCTTGGAGGATTTCAAGCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAAAGTCCCAAGC
 CTTCCTTGCCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATCTT
 ACATGGACAGCACCAGGAGATAATTTGATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGAAGTATTTCTT
 GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGAGGCCAACTCCAAGGAA
 AGCTTTGCATTTAAACAGAAAAATATCTCAGAAGAAAATGCAACCCACATATTTATTGCCATTTAAAGTATAGATAAA
 AGCAATTTGACATCAAAAGTATCCAACATGCAACAAGTAACTTTGTTTATCCCTCAAGCAAAATCCTGATGACATTTGAT
 CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTTGGAGTTAATATTTCTACGCTGGTATTG
 TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC
 AAGTAGACCTAGAGAGAGTTTAAAAAACAAAAACAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT
 GTGTGATCATAACTCATAAAAATAATTTAAGATGTCGGAAGGAGGATACTTTGATTAAATAAAACACTCATGGATA
 TGTAACAACTGTCAAGATTAATTTAATAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTATGAACAAAG
 ATCCTTTTTCATCTGATACCTGGTTGTATATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA
 GAAATTAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAATTAACAACATTTGAAAAAATAAAAAA
 AA

FIGURE 70

MGLFRGFVLLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE
ATEKRFFFKNVSIIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR
MNQAAKHFLQTVEGWSVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNMGVYSRYFTAYTENGRYSIKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPP
RPEIDEDTQTTLDEFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIILTWAPGDN
FDVGKVQRYIIRISASILDLRDSFDDALQVNTDLSPKANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCTCCCGGGCAGGGGTGA
CAACAGGTGTCTATCTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCCTCTTGCTGTTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCCCTGCAAGATCATCTTTAAA
AGTAGAGAAAGCTGCTCTGTGTGGTGGTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTTTCGCCGGGGGCTGCTTGCCTGGATTTCCCGGGTGGTG
GTTTTGCTGGTGCTCCTCTGCTGTGTCTCTGTCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAG
CTGGCACTGCCAGGGCCAAACAGCCACCGGGGAAGGAGGGGTACCAGGCCGTCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG
AATGGCAGTACCAAGCCAGCGATGCTGTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAACCCAGGCCACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGACGACGTG
CCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGCAAGCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACCCTGAACAATCCTGCAGAGAACAGC
CCCAATCAACCTCTTACACGGCCTCTGATTTTATAGAAAGGATCTACCGAACAGAAAGGGACAAGGGACATTGTAT
GAGCTCACCTTCAAAGGGGACCAACACGAATTCAAACGGCTCATCTTATTTGACCAATTCAGCCCCATCATGAAA
GTGAAAAATGAAAGCTCAACATGGCCACACGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAAGTTT
CGGCAGTTTCATGAGAATTTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAGAAATAAATGAAGTCAAAGGAATACTTGAACACTTCCAAGCTGCCAATTCAGGAATTTTACCTTCATC
CAGCTGAATGGAGAATTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGTCCTTCTC
TTTTTCTGTGATGTGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG
GATTTTTATCCAGTTCTTTTCACTCAGTACAATCCTGGCATAATATAGGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTGGATTTGGGATGACGTGTGATATCGGTGACAC
TTCATCAATATAGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGAGCGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG
GTGTTCAAGCAGGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGACAAGTAGCAAAAAACATGAACCTCCAGGA
GAAGGATTTGGGAGACACTTTTTCTTTCTTTTGCATTAAGTGAAGTGGCTGCAACAGAGAAAGACTTCCATAAA
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTTACAAACAGA
AATCAAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTGCACCCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGA
AATATTCAATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACT
AGTGAGTACATTAAGTAAATAAAATGGACCAGAAAAGAAAGAAACCATAAATATCGTGTATATTTTCCCCAAGAT
TAACCAAAATAATCTGCTTATCTTTTGGTTGTCCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCAGT
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCAAGTTGGCCTAC
ATTTTTATATTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTGATGCCATAT
CCAAGGACATGCCAATGCTGATTTCTGTAGGCACTGAATGTCAAGGCATTGAGACATAGGGAAGGAATGTTTGTACT
AATACAGACGTACAGATACTTTCTGAAGAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTTCTGCTTTACAGAAAAGGAACTCATTCAAGCTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACTTTT
CTCCTCAGAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCTTTTC
AAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAAGAAATGGAGAAAAATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGGAAG
TAACTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATTGCATTTTATTACCATTT
CAAATATTTTTTAAATAAATACAGTTAACAATAGAGTGGTTTCTTCATTTCATGTGAAAATTATTAGCCAGCAGCAG
ATGCATGAGCTAATATCTCTTTGAGTCTTGTCTTCTGTTTGTCTCAGATAAATCATTTGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTGTACTGGTAGTTTATGAAATTTAATTAACACAGG
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTGTGCATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIESALETNNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLF
SQQY
NPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTQYRSDFINIGGFDDIKGWGGEDVHLYR
KYLHSNLIIVRTPVRGLFHLWHEKRCMDLTPQYKMCQSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

[illegible]

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTDPDLPALQ
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTGACAGCTCC
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTGATGGAAATTTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGA
GCTCAGTTTGAGGAGGAGGTGTCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTGGTCGACTGGGA
TCCCCAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTATA
TGTGCAGATGGAAAACTGATGGCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTTCTTATTCTCATAGCACGTGTGTGATTGGTTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGTTGTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSIISVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHANLILYGNFDRFFVPAEK
IVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPDKTVIEYDYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQ
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCGAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCCTCAGTCCCAGTTCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC
ATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
CCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACCTGCTGTA
TAAGTCTCTCTTCTGGTGAACGCCTTAGCTAAGCAGGTATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
TCCTGCCATCAAGGGTGACACCATTACAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCTGACAATGCCACCCTGGACAACATCCCG
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
CCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
TTGTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGG
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILQQLPLLSAMREK
PAGGIPVLGSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYLGAKLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSVGVPSLVKALG
FEAAESSLTkdALVLTpasLWKpSSpVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCAGGCATCACCCAGTGTGACATCTATAGC
ACCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCT
ATTCTGTGGCTGGAATCTTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAATACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCTACAGCCTGACAGGGTATGTGTAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAAGTGAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVG YILG LLLG LTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFI PVAWN LHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFN SYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTTCCT
GCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCTGTGCCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
ACCAGCGGCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTCTCCTCCTTGCTGGGA
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCTGATGT
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
GTTCACTGCCCCAGCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGCCCCACCAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCGAACCAGGCTGCCAGCACCCCTCCC
ACTGCCAGACTCCTGTGCCAAGCCTGCAAGATGAGGCAAGTGAAGAGGACA
GTGTGCAGTGCCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAG
AGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAAGTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGG
ACAAAGCAGACCCTGGCCACAGTGAATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCAAGCCAGACAACCTGCGTGCCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT
GGAACGTCTTCTAGCCAGACCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATATTAATAAA
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHYPYLEPQGLMYCLRTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYS
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTFYPCRHPKAVAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPARRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCACAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTGACACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTGAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGTTACAGATAG
GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAACCTGGACTG
GAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
ACATTAAATCCCCGTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG
TGAGTCTCTCTCACAGGCAACCCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTNSSESSQATTFFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCCT
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCTGACCCCTGTGCCCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAG
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTC
AGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCCTGATTGAGGGATCACAGCCCCCTCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPACEQGTTPMISWIGTSVSPLDPSTTRS
SVLTILIPQPDHGTS LTCQVTFPGASVTTNKT VHLNVSYPQNL TMTVFQGDGT VSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVS LQSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGD TGIE
DANAVRG SASQGPLTEPWAEDSPPDQPPASARSSVGE GELQYASLSFQMPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCACTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTTGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCATAAGTCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCAGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGCTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTILVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIPIVVYDFGDAQKTASYISPYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPOCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCTTCTTCAT
ATTTCGAGCGTTGGGAGTGCACGTATTGGTACATTTTGTCTTCTGCAGTGCCCTTCAGCTG
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAGAAACCCTTCTTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALEFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTTGGTGACGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCAGCCCCC
CACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTAC
CATAGTGATACCCCCTACTACCATCTGGGTGACCCCGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTTCTCCCGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTCTGAAAATCCCTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVSGLGFGIMSGV
FSFVNTLSDSLPGTVGIHGDSPOFFLYSAEMTLVIILLHVFWGIVFFDGCEKKKGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAACTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAACA
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
CAATTTTGTACACAACCTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCACAGCAGGCCGCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTCAAATTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGAAAACCTGGAAAAA
AA
AA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDLLHLLNPAAGMTPTGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLLIHSLEFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

10063711

FIGURE 97

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCAATG
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCAGAAAATATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCGCTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTCAACCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCTGTGCTGTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGTGAGCCGGGGTACCAGGCCTGGCATCCCCCTTCCTCTTCCTTGAGGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCTCAGGCCACAGGCCACTGCCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGT
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGCACACATGGCCAGGTA
 CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAA
 TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAATTTCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCGGCTCCCCCA
 ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
 TCGAAGTCGCAGTCACAGATATCAATGATCAGCCCCCTGAGTTTCATCACTTCCCAGATTGGGCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCACCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTTCCTGCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
 TACCTCTGCACACCCCGCCAAAGACCATGGCTTGATCGTGAGTGAGCCAGCAAGGACCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT
 GAACACATAATCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTTGAGTGTAT
 CGTGTGTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCCTC
 ATTTTACCCCACTGGACCATGTCAAGGAAGAAGGACCGGATCAACCAGCAGACAGCGTGCCCT
 GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
 TCCCTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT
 TATGGACTGCCCATGGGAGTGTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQFVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSIESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVEVNAEENLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTGTFGLDWEPSGHVRLRLCKNLSY
EAAPSHEVVVVVQSAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRQLTLNGSHAYLTALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTTLVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCTG
AGTCCAAGATTCTTCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
TCTCTTCACTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC
ATCTAGGACCCAGGCATCTTGCTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
TTCTCCTTATGTTTGGTCTACTATTGCATTAGAGCTGCAACAAATTCCAATGAGACTAGCACC
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
GCATAGTCACCAACTCTGAGTTCCATACAACTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACAGTCACCAACT
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCC
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
TCCAGCACAGCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGG
GGTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGCACAGCCACCAACT
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCTCC
AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCC
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
ATGCACACAACCTCCCATAGTGATCTACTGCAGTGTGAGGCAAGCCTGGTGGGTCCCTGGT
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGCCGTGGGGCTCTTTGCTGGGC
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT
CATGGCCTCAACCATGGCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCACAGGCCCAG
GTGGAGTCTTAAGTGGTCTGGAGGAGACCAAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
CCCAAGACCTGGTTTCTTTCATTTCATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA
AATCTTGAAGAAGGTATTCCTCACCTTTCTGCCTTTACCAGACACTGGAAAGAGAATACTATAT
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACAGACAAGAGAAGCTGTGCTTG
CCCCGGGGTGGGTATCTAGCTCTGAGATGAACCTAGTTATAGGAGAAAACCTCCATGCTGGACTC
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTSSGASTA
TNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTSSGASTATNSESSTSSGASTATNSDSSTSS
GAGTATNSESSTVSSGISVTNSESSTPSSGANTATNSESSTSSGANTATNSESSTVSSGASTA
TNSESSTSSGVSTATNSESSTSSGASTATNSDSSTSSSEASTATNSESSTVSSGISVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLEAGLFFCVRNLSLRNTFNTAVYHHPGLNHGLGPGPGNHGAPHRPRWSPNWFWRPVSII
AMEMSGRNNGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTACAGGTG
GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGATGGAAAGGGATTACTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGGGAAGCATT
TCATGCTGAGTCCCTTTTACCTTTGATGTTGTAAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAAGT
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTCTATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGTTGGTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTATAGGAAATGGAAGGATGACAAGAGCCATTTCAAGACATGATTGATTACTTTTGTG
ATATTACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACACATTCTCAATCAGAGAAGCACCTCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTTACGTCCACCGGTATCCAATAGACACCCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCTTCCACCTTGCAAGTCTGAAGTCAAGGTC
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAATTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTT
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAACAATCATCAGGCTTTTAA

FIGURE 102

MHSRGREIVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFMLSP
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCLMRYSYLRLEKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLQGDFFPREIHFWHRYPIDTLPTSKEDQLWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRLVVKLLSILYWTLESPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
LEIIEIACRYRLHKKPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTGTCCAGGCCTTGGTGGGGGAGGACGCGTGTCTCCTGCTCCCTCT
TTCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGCTGGCAGCACTGGGCTCACTTCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGAATCCAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGGCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAACGTAAACCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGGAAGACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTT
ACATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTCAAGTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATTATTCATATGTCCAGTGTCTCGGGATGAGACAGAGAAGACCTGCTTAAAGGGC
CCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCCCGACAGGTGGCCCCAGCTTCCTCT
CCGGAGCCTGCGCACAGAGAGTCAAGCCCCCACTCTCCTTTAGGGAGCTGAGGTCTTCTGCCC
TGAGCCCTGCGACAGCGGAGTCAAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCAACCTCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCTGCCTCAGGTTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGAGGTT
TGAGGGCACAGTGTGTTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTT
TGCTTATTCACATTAAATTTACTTTTCTCTATACCAATCACCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCAGCAT
TACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
CTCATTAACACAGACACAAAATTTAAATAAAATTTTAAACAATTAACATAAATAATATTTA
AAGATGATATATACTACTCAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTAATATTTAAAT
ATCAACCAGTGAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAPOEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGCTGCGCAGTGTGCATTGGA
CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
TGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA
AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGTCTCACTGTTTACAAATATAAGAACCCTGCCAGATGGACTGCTTCTTTGGAGTAACA
ATAAAACCTTCGAAAATGAAACGGGGTCTCGGAGAATAATGTCCATGAAAAATACAAACACCCATCACA
TGAATATGATATTTCTCTTGCAAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGT
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTTGAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTG
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTG
GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
ATAAACTGTTTGCTTGATGCATGATTTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
GATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTTCATTTGTTCTCTAGAAGTTTTGTGCAAAATTTGACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTAGCAAAATATCCATTT
TCAAGGTGCAGAACAGGAGTGAAGAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACA
GCAGATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAAGTAAGGAAGTCCAGAAAGAAGCCAAG
ATATATCCTTATTTTCATTTCCAACAACACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAAACATTG
TTACTGAGGATGTCAACATATAACAATAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPREEFVKSQVIFSQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSPVYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCTG
 CCCCAGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCCAGC
 GCCGACGATCGCTGCCGTTTTGCCCTGGGAGTAGGATGTGGTAAAAGGATGGGGCTTCTCCCTT
 ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCT
 GTGGTTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCTTATCATTGTGGGGATGTTAGGATATTG
 TGGAACGGTGAAGAAGAAATCTGTTGCTTCTTGACATGGAACAGGAACCTATGGTTCCAGTACAATGGTCA
 GATATGGTCACTTTGAAAGCCAGGATGACAAATATGGATTACCTAGATATCGGTGGCTTACTCA
 TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG
 AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTAGAGAAATCCCAGGATGTTCCAAA
 CAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCTT
 TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG
 ACAGACCAATGATGTCTTGAAGAATGACAACCTCTCAGCACCTGTCTATGTCCCTCAGTAGAAT
 GTTGAAACCAAGCCTGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
 TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACT
 TGTGAATTTTGTAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA
 TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCTAAGTC
 ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCGCA
 TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
 CTCAGCGATCTATTCTTCTGATGTAAATAAATTATATATCAGAAAACCTTTCAATATTGGTGACT
 ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACCTAAAAGAGCAAGCTAACACAT
 TGTCTTAAGCTGATCAGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCACTCGAT
 TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT
 ATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC
 TGTATTTTAAATACTTAACCACTAATTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA
 AAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA
 GCTTATCTTTGCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATCTACAGAAAA
 TAGTGTCTTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATT
 CTTTGTTTTATTCTACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTAT
 TTCTCAGAATATGGAAGAAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNVLTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPQTDQM
MSLKNDNSQHLSCPSVELLKPSLSRI FEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGATAAAGCCCCCTACCAAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAGTCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCCCTCCATTCTCTGCTTCTCACCTG
CCTCTTCATCAGGCACCTCCGTGTACCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACAGTTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTGGCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATCGGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCCTACCGCTGT
GAGTGTGGGGTGGCCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGTGT
CTGAGGATAACCACTTGCCAAAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCAGCCATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
ACCTGCCAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT
CATGAGCCGAAATCATGGGATCTTCCCATTCCTGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCAGTGAGCGGC
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTCCTGCACTGCCGGGTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTGGCCACCGGGAATGCCGCTGCTGGGCGAGGAGGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTTAAGAACATCTGCCAACAGC
TGGGTTGAGACTTCACACTGTGAGTTCAGACTCCAGCACCACCTCACTCTGATTCTGGTCCATTGAGTGGGCA
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAACTGTCCA
CCCAGAAAGACACTCACCCCATTTCCCTCATTTCTTCTACACTTAAATACCTCGTGTATGGTGAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAACAGTTACTGAAATTATGA
CTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAATTTCAATTCAATGCAGACTAA
TTATAGGAATTTGGAAGTGTATCAATAAACAGTATATAATTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSEDNHTCQVPVLCKSNAIEVNIIPRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEEPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYILIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGGCHRRMRGAGGEDSAGLQGGTLTGGPIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCCGAAACCCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
GGTTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
AGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
GAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTG
TGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCA
GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAGACAATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTCCTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCCCTGATGTACCAATCTGACCACTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTAATGCTGCTGCCCTTTGCACTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGACCAAGAGTCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
TTCTTGAGACAGCAAAGGGCCTCAATTCCTGTAAGAGACCCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAGGGTCTGCCAGCCCTGTCCGTCTTACCCATCCCCAA
GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
AAAA

FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAEATACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL
GSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSSGGLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAACCTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC
TGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTATAGGCGATGGCTCCCACTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCAGCTGCCCGCCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTTGTCCAAATTATGGGTGAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA
TGGTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLPKPDHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCTT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAAGTAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIFYVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLE
ERGYCCIIYCRGNRYCRRVCEPLLGYYPYPICYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGGCGGGCGGGCAGGATCATGTTCCACCACCACATGCCAAGTGGTGGCGTTCCTCCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAACATGCTGGTGACTAATTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTACAGCAGGTACACATTTGGTGCAGCTCTGTTCTGGGCTGGGTGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCACGACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAACA
GCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTAACTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCAAGAAAACCTTTGAAAGGAAA
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTGAATTTTGTCTCCCCACCCCAACTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAGTTACCAAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAGTCCTCTTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCA
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGGGAGTCC
AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGCAGAGTGTGGCCTTCATT
GAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACTTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAGTCAACCGAGCG
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGAGAATGAGATA
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
ACGACATAGCATTATGTACATAGATGAGTGAACATTTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
TTTATAATGAAGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
CTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
AAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA
TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
GCTCCTATGTGGGTACCTGAGTCAAAATTTGTCATTTTGTCTGTGAAAAATAAATTCCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATCTGTATTTTCTGTTTATTCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
TATACATTTATATTAATAAATTGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK
IYDSL LALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGGCGGCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGCGAGCC
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCGCAGCGGCTCCGCGGCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCCGCGCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTGGGATCCCAGGTCCGGATG
GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGATACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAAATGCA
GAAATGCATGCTGTGAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGTGCTGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTCTCTTAGTATAGCATTTTAA
AAAAATATAAAAGCTACCAATCTTTGTACAATTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRIS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
 CTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
 ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
 ACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
 TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
 TGTTCCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
 TCTTCCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTATGCAACTG
 GCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
 CTTTCTTCTGCGGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
 ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
 ATAACAGCCTTCAAAAAGTAAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
 CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGA
 GCTGATTCTTAGTTCCAATAGAATCTCCTATTTCTTAACAATACCTTCAGACCTGTGACAAAT
 TACGGAAGTTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
 CGGAAGCTGCTGAGTTTACATTTACGGTCTAAGTCCCTGAGAACCATCCCTGTGCGAATATTTCCA
 AGACTGCCGCAACCTGGAAGTTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATG
 TCTTTGCTGGCATGATCAGACTCAAAGAAGTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
 CTGGCCCTTTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGT
 CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
 TCGAAGCTTTTCAAGTGGACCCAGTGTTTTCCAGTGTGTCCGAATCTGCAGCGCTCAACCTGGAT
 TCCAAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
 TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTT
 TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAATGTG
 ATCGATGCAGTGAAGAAGTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
 GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCAAGGCGGAAGCATGAGAGCAAACCCCTT
 TGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCATCTCT
 TTCCATAAAATCATCGCGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
 CTACGTGTGATGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
 GGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA
 GATTATAAACCACCAACACGAGAGACCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA
 TAACAAATCGGGCTCCAGGGAGTGTGAGGTATCAACCATTTGTGATAAAAAGAGCTCTTAAAGCT
 GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCTCCCT
 TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTTCATAACT
 GGTCAATTTCTCTCATACATAATCAACCATTTGAAATTTAAATACCACAATCAATGTGAAGCTT
 GAACTCCGGTTTAAATAATACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCGATTT
 GTTTTAAGATAAAAGTCTTTTCATAGGTAAAAAAGAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDSLQNQLHSLGSEQFRGLRKLKLSLHLSNSLRTIPVRIFQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCITYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGGCTACTGCTGAATGTCCTCCGTCCTGGAGGAGGAGGAGAGGCTTTGCGCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGCAAAAGTGAAG
ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAAATGGAAGGAAAAGGAACTGGAAGG
AAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAGCAGAATAATGAATCAACCACGAGATAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMOMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGCGGAGAGCGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCTACAGATGTGACCTAT
CAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCCGGCCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAAACATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCCTTCATGGCTTGCCCTCCTGCTCTGGATTTTAGGTGTTGATTCTGGAT
CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGTCGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCAGTCTTGCTTCTTGTCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININSMGHRVLPVSVTHFYATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AAC TTCTAC ATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTT CAGGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAAC TTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTT CATTTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAAT TGAGGAACTGAGAAAATTAATTTCTCATGTATTTTTCTCATTTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTGCCTCGGCCTCCCAAAGTGTATGATTACA
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAAC TTTGAAATTAT
ACAATGAATTATTGTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTGCTGCAAAATGACAGGATTTTCGTTCTTAATTTCAATTAAATAACACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGGHTLGESPMFPKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACCTCTTACCTTCAGAACACCAAATAAATAATGCTGGGATTCTTTCAGAT
TTGAAAACTTGCTGAAAGTAGAAGAATATACCTATACCACAACAGTTAGATGAATTTCTACCAACCT
CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA
AAATTCCTTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTATCACCATCTCTCAAG
GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGGGAATTCCCTGACTGCTGCACCAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCTCCCAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTCTGTTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATATCTCTTGAAACTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCTATAAAGTATGCATGGTTC
CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT
CGAATGTACAACCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG
TTCATAGGAATGGATCGCTCTTCTCAAGGAACGTGTCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCATATTTCTCCTAATGGAATGAATCTGT
ACAAAAACAATCAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL
EELHLDNSVSAVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLT AAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQQQWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKS VTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSPYKVCMPMETS NLYLFDETPVCIETETAPLRMYNPTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIAL LALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSESSSNRSYRDSGIPDSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGCA
GCCCTGCCGGGCCACTTGTCTTCATGCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCCTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGGTCCGAGTCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCCG
GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGC
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
GACAGCAGCGAGCCCTGCGGCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
AGGCTACTGCCTGTCCACCAACTGCTCTTCTTCTCTGCGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGCCATCGGATACGCTACCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
TGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC
AATTCTCTTGCCTCATCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
TTTTATATTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTGGGATTATTAGGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACCCATCCACACCG
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACCCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 134

MSARGRWEGGGRRACRGSGLARAQGAERTVSSEQRPMASLGLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSSSEPCGLSDLCSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIEMENIMFCGMMGFSDFYKLRWLEAILSQKQOEGCFG
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCILIP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT
AACTTTTGTAGCATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPQDWISAA
RVLVDGEEHVGLKTDGSFVVDIPSGSYVVEVSPAYRFDPRVDITSKGKMRARYVNYIKTSE
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLIFVLLPKVVNTSDPDMRREME
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTKGSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAACAA
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAC TAGACATTCTTCTGCAATGGATGGAGGAGACAGAA TAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGATCTTATTTATGCATTACTTG
CTTCCTTGCAATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA
ATGTATTTATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAAAACCTTGTAATTC TAGAAGAGTGG
CTAGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTGATGTGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTGTATCTCCAG
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAA
AAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF
SSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42.

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC
 TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
 TAGGGATCGCGGTCTTCCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCCAGAGCGGAA
 CACGGAGCGGAGCCCCAGCGCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAAAAAGGAGCATCTCACAGT
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
 CCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
 TAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
 TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGT
 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTCAGGGCCCAACAGCCCCCTGATTGGGCGAG
 AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA
 GACGCTTTTACCAATTGCTGGTCTTTGTTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
 GGGCTTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAA
 CCCGGTGATATCCGACATCCAAAGCAGCTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
 ACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGAC
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG
 AATGTCCGTCATATGAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTATTCAACCTGGGCTCCAAGG
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG
 TTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA
 CTGTCACTCTCTGGGTTTTCTCTGCTCTTTATTTGGTGATCCTGGTCTTTTCGGCCGTTACGCT
 CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCTCTCGTGGCTGGCGGCAGGCT
 GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCCTGGAC
 AGGGGGCTCAGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG
 TTCACATCTGTGCTGTGTCAGGTGAGATGCCTCAGTTCTTGAAAGCTAGGTTCTGCGACTGTTAC
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
 TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
 CACTCAGGAGGGTCAAAGGAGACTTGGTGCACCACTCATCCTGCCACCCCAAGATGCATCCT
 GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCCTTAGTCCTTGGCC
 TCGGACACCTTCATTGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
 ACTCAGATCCACAGAGCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
 ACCCAACCCTGCACAGCCCTCATCCCCCTCTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGT
 CTGACCGAGACACTCACAGCTTTGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAG
 CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHVEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAACCTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTCTGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGGAGTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTGAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																					
101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 33-36

Interleukin-1
amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACAGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTCGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA
AA

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTTCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLGEGH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTGTGACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTTACAGATAAGGAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSWWLATVCMLLFSHLSAVQTRGIKHKRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT
CCTGATGATTTATAGACTCAAAGAAACTCATGTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCACTGAGTCTTAGTTTTATTTTTTGAAATTT
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGTGCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLFLLLISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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FIGURE 149

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCC GCGCGCCCAACCTGCTTATCCCTTGACCGTCGAGTGT CAGAGATCCTGCAGCGCCAGTCC
CGGCCCTCTCCCGCCACACCCACCTCCTGGCTCTTCTGTTTTACTCCTCCTTTTCATT CATA
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACTTGATTCTGGTGT TAGTGCTCCCGATTCAAGCTTTCCCCAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAACTG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCACAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGAAAGGAGAACTAAAACCTACAGTGAAGACAACTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAAAAAGAAGCAAAAGAGAAAGAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVT PMAAIQDGLAKGENDET VSNLTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNKLEKNATDNISKLF PAPSSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEAIAKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
 GATGCTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
 ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
 GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCTGGGTGTCCAGGGTGGAAG
 CCAGTGCCTGTGCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
 AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC
 TCCAGCTTCGAGTCCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCC
 TGTGAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
 AGCAGTGTGACTAGGGCAACGTCCCCCGAGAAGTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
 GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG
 TGGGCACCTGACCCTTTGTCTTCTGGTTCCTCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
 CCACGGTCTCCCCACTGGATGGTGTCTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAA
 CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCT
 TAATGGTAACTGACAAGTGTACCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA
 GGGTCAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
 GAGTCAGGGATCTATGGCCCTTGGCCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCATA
 TGCTACCTTTCCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTGTCAGAA
 GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
 GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGA
 AGACCTACTTACAAAAGTGGCATATATTGCAATTTATTTTAATTTAAAGATACCTATTTATATATT
 TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT
 AGGTGATTTTCTTTTAAATCTGTTAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGA
 ATTCTTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
 TTGTCCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
 TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
 GTGGCTGGAATCTCTGGGTAAGGAACTTAAAGAACAAAAATCATCTGGTAATCTTTCCTAGAAG
 GATCACAGCCCCCTGGGATTCCAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
 ATGTGTCCCCCTCAAATTCACATCCTTCTTGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG
 GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATAT
 GACTGGTTTCCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
 AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
 ATCAGAAGCTTGGAAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
 CTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAAAGAATAAATTCGGCTGTTTTAA
 GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT
 CTCCTCGTGTTTACATTCTGTGTGTGTCCCTCCCAATGTACCAAAGTTGTCTTTGTGACCAA
 TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
 TACTTGAGCCCTCTCTCTGCCACCCACCGCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
 AAGCTAGCTGCCATGCTATGAGCAGGCCATATAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
 GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
 AAGTTGCTCAGTTTTGGTCTAACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESVVPNRWLDASLSPVILGVQGG
QCLSCGVGQEP TLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENG GWNAPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

APP ID=10063711

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTCTGTCTATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTTGAAGAAGTCTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGCCTTCCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACCAAAGGAAGATGGGAAGCCAAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTGTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTCAATTGTAAGTGGTGTTT
TATACACAGAAAAAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTATTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLLIGEKLFGVSMSERCYIMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCGACTTGTGACTGAGTGTGAGTGCCAGCATGTACCAGGTCA GTGCAGAGGGC
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCCGT
TGCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCAGCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCTGTGAAGTGCTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAA
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCCTCTTTTCCCATCCCCTGCTACCCTG
GCCCAGCACAGGCACCTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCTGGTTTTATT
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACA
GTAGAAGTGAAC TTCACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGATAGTGAAGGTGTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTC TTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGCTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLDLRLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMYKKKCKAGSLWDPNITACKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPPFLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGFPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQVVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGAAGTGTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 16o

MTVKTLHGPA~~M~~VKYL~~L~~LSILGLAFLSEAAARKIPKVGHTFFQKPESC~~P~~VPVGGSMKLDIGIINEN
Q~~R~~VSM~~S~~RNIESRSTSPWNYTVTWDPNRY~~P~~SEVVQAQCRNLGCINAQ~~G~~KEDISMNSVPIQ~~Q~~ETLVV
RRKHQGC~~S~~VSFQLEKVLVTVGCTCVTPV~~I~~HHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

A C A C T G G C C A A A C A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A G G
 A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G A T T C
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C T T G G G G G G G G C A G C A C
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T G C C C T G G T T C T T G C T G T C C T
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G T A C C
 C A C T G C T C T C C G G G C C T C C T G C C C C T C T G G G A C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T
 C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C
 A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C C G T G C A T G G G C A C T G G
 G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G A G C C T A G G A A
 T G C C T C T C T C C A G G C C C A G T C G T G C T C T C C T T C C A G G C C T A C C C T A C T G C C C G C T G C G T C C T G C
 T G G A G G T G C A A G T G C C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C
 T G C T T C G A G G C T G C C C T A G G G A G T A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G T G A C A
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A C T G G A A T C A G
 G T C C A G G G C C C C C A A A A C C C G G T G G C A C A A A A C C T G A C T G G A C C G C A G A T A T T A C C T T G A A
 C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A
 C G A A C A T C T G C C C C T T C A G G G A G A C C C C G C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G
 C G A C T G C T G A C C C T G C A G A G C T G G C T G C T G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T
 G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G C C A G C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G
 T C A C T G T G G A C A A G G T T C T C G A G T T C C C A T T G C T G A A A G G C A C C C T A A C C T C T G T G T T C A G G T G
 A A C A G C T C G G A G A A G C T G C A G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A
 C G A T G T G C T A C T G T T G G A G A C A C A G G C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A
 G T G G C T G T A C T T C A C T A C C C A G C A A A G C C T C C A C A G A G G C A G C T C G C C T T G G A G A G T A C T T A C T A
 C A A G A C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G
 C C C C A T G G A C A A A T A C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G
 C T G C G C T T T C C C T C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A
 C A G G A C G T C C G C T C G G G G C G G C C G C C A G G G G C G C G C G G C T C T G C T C C T A C T C A G C C C A T G A
 C T C G G G T T T C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G
 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G A G G G C C C G T G G C T T G G T T T C A C G C G C A G
 C G G C C C A G A C C C T G C A G A G G G C G G C G T G G T G G T C T T G C T C T C T C C C G G T G C G G T G G C G C T
 G T G C A G C A G T G G C T A C A G G A T G G G G T G T C C G G G C C C G G G G C G C A C G C C C G C A C G A C G C C T T C C
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C C C G G C A G C T A C G T G G G G
 G C C T G C T T C G A C A G G C T G C T C C A C C C G G A C G C C G T A C C C G C C C T T T T C C G C A C C G T G C C C G T C T T
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C G C G T T C C G
 G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C
 C A T C C C C G G G G A C T C C C G C G C G G G A C G C G G G T G G G A C C A G G G G C G G A C C T G G G G C G G G G A
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T C T A A A A A A

FIGURE 162

MPVPWFLLSLALGRSPVVLSELRLVGPQDATHCSPGLSCRLWDSDIILCLPGDIVFAPGPVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTQAYPTARCVLLEV
QVPAALVQFGQSVGSGVVDCEAALGSEVRIWSYTPRYEKEINHTQQLPALPWLNVSDGDNVHLVLNV
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQLECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLYSADDGSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCACAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTACGCGGATCACCCGGAAGTCCTGC
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
GTCAGTGCGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTAGCTCTCTGCAGCACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTAGATGATTGTTTCATCCTA
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCCCTGGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTGCGTTTCCCA
CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCTCTCGTCGAGTACTCTGCTACCTGAG
CTACAGATATGTCACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTTGACTT
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTGACCTCAGCGGCCCCAGC
AGTCTGGCCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACTACTTAGGGCAGCCAGACATCTCCATCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCTCTCCCCACTGTCTATGCCCCAACGCTGCCCTGAG
GTGGGGCCCCATCTATGCACCTCAGGTGACCCCGAAGCTCAATTCCATTCTACGCCCCACA
GGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTCTAAA
CACCTTAGGCCTAAAGGTGAGTTCTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGCGCT
TTCTCTGCAGGAGGTGACCTCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGTCCCCCTCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG
GAGCAGCCCCACAGAAGTGGATTCTCTTTTTCAGAGGCTGGCCCTGACTGTGCAGTGGGAGTCTTG
AGGGGAATGGGAAAGGCTTGGTGCTTCTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG
CAAGGCAGAAATGACAGTGAAGGAGGAATGCAGGGAAACTCCCCAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTGGCCGATTTC
ACAATCTAGCTCGACAGAGCATGAGGCCCCCTGCCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAGAACAACCTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCTGCAGCTCA
TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCAATTCCTCTGATAGAACAAGC
GAAATGCAGGTCCACCAGGGAGGGAGACACAAAGCCTTTCTGCAGGCAGGAGTTTACAGCCCT
ATCCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC
TGTAATGATGTACAACCTTTGCAAGCTCTGCCTTGGGTTAGCCCATCTGGGCTCAAATTCAGC
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCTC
ATCTGTAATGTGGGGATCATAACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTELYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSIAM
EESQEAKSLHQPLGICTDRTSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHMSLPLQPPSGPC
SPSDQGPSPWGLLESIVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA
AGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGACTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGCGTGA
ACTTGACCTGTGCCTGAGCCCAGGCATTGAGAGCTGATTGAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATCTGCACGATAA
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT
CATTACAGCAAAGGATTTGTTGGCATCAAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGATTTTTGAGCCAAACAAAATATATTATTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFWL GALWWVPGQSDL SHGRRFSDLKVC GDEEC SMLMYRGK ALEDFTGPDCRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADETFVCFEGGRD
DFNSYNVEELLGSLLEDSVPEESKKAEEV SQHREKSPEESRGRELDPVPEPEAFRADESDEGEA
FSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSGKGRFWHQNLSLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

CAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
 AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAACTTC
 AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
 CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGCTCGGGC
 GCGGGGAGTAGGGCCCGGCAGGGAGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
 GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
 TCTCGCTGCTGCTGGGCGCCGCGTCTGCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTTCAGC
 GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
 GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCTCTCTCA
 GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
 ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG
 TGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATTCCCAGTACCGAAACTGGTACACAG
 ATGAACCTTCTGCGGAAGTGAAAAGTGTGTGTGATGTATCACCACCAACTGCCAATCCTGGC
 CTTGGGGGTCCCTACCTTTACCAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
 CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG
 GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
 ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT
 GCATAAAAGTAAAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
 CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAATTCT
 GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGC
 AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTCA
 TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
 ACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
 TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTTACCTTTTATAAGTTGTTATCTAGTCAATGTAA
 TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA
 ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAG
 AAACCTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
 TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA
 AATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
 TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTAGCTTAAATTAACAGATT
 TTGTAATAATGTAACCTTGTGTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
 TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
 GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG
 ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
 ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
 ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACTACGAAATCGTGTGAAAATGGGTGG
 AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTT
 CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCT
 CTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTTCTTGTGTTCTGGGGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFCRVVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-
145, 212-217